

B. Mayhew

1652

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/371,347
DATE: 05/05/2000
TIME: 12:14:22Input Set : A:\seqlist.txt
Output Set: N:\CRF3\05052000\I371347.raw

ENTERED

4 <110> APPLICANT: Roy A. Gravel et al.
6 <120> TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
7 CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
8 DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
11 <130> FILE REFERENCE: 50004/003003
13 <140> CURRENT APPLICATION NUMBER: 09/371,347
14 <141> CURRENT FILING DATE: 1999-08-10
16 <150> PRIOR APPLICATION NUMBER: 60/071,622
17 <151> PRIOR FILING DATE: 1998-01-16
19 <150> PRIOR APPLICATION NUMBER: 09/232,028
20 <151> PRIOR FILING DATE: 1999-01-15
22 <160> NUMBER OF SEQ ID NOS: 51
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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27 <211> LENGTH: 2097
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
31 <400> SEQUENCE: 1
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33 gaaatgtgtg agcaagctgt ggtacatgga ttttctgcag atcttcactg tattagttaa 120
34 tccgataagt atgacctaaa aaccgaaaca gctcctcttg ttgttgtgtt ttctaccacg 180
35 ggcaccggag acccaccgga cacagccgcg aagtttgtta aggaaataca gaaccaaaca 240
36 ctgcccgttg atttctttgc tcacctgcgg tatgggttac tgggtctcgg tgattcagaa 300
37 tacacctact ttgcaatgg ggggaagata attgataaac gacttcaaga gcttggagcc 360
38 cggcatttct atgacctggt acatgcagat gactgtgtag gtttagaact tgtggttag 420
39 ccgtggattg ctggactctg gccagccctc agaaagcatt ttaggtcaag cagaggacaa 480
40 gaggagataa gtggcgcaact cccgggtggca tcacctgcat ccttgaggac agacctgtg 540
41 aagtcagagc tgcacacat tgaatctcaa gtcgagcttc tgagattcga tgattcagga 600
42 agaaaaggatt ctgaggtttt gaagcaaaat gcagtgaaca gcaaccaatc caatgttgta 660
43 attgaagact ttgagtctc acttaccogt tcgggtacccc cactctcaca agcctctctg 720
44 aatattcctg gtttaccccc agaattttta caggtacatc tgcaggagtc tcttggccag 780
45 gaggaaagcc aagtattctg gacttcagca gatccagttt ttcaagtgc aatttcaaag 840
46 gcagttcaac ttactacgaa tgatgccata aaaaccactc tgctggtaga attggacatt 900
47 tcaaatacag acttttctca tcagcctgga gatgccttca gcgtgatctg ccctaaccagt 960
48 gattctgagg tacaaagcct actccaaaga ctgcagcttg aagataaaag agagcactgc 1020
49 gtccttttga aaataaaggc agacacaaag aagaaaggag ctaccttacc ccagcatata 1080
50 cctgcgggat gttctctcca gttcattttt acctggtgtc ttgaaatccg agcaattcct 1140
51 aaaaaggcat ttttgcgagc ccttgtggac tataaccagt acagtgtgta aaagcgcagg 1200
52 ctacaggagc tgtgcagtaa acaaggggca gccgattata gccgctttgt acgagatgcc 1260
53 tgtgctgctg tgttgatct cctcctcgtc ttccctctct gccagccacc actcagtcctc 1320
54 ctgctcgaac atcttcctaa acttcaaccc agaccatatt cgtgtgcaag ctcaagttaa 1380
55 tttcaccag gaaagctcca tttgtcttc aacattgttg aatttctgtc tactgccaca 1440
56 acagaggttc tgcggaaggg agtatgtaca ggctggctgg ccttgttgtt tgcctcagtt 1500
57 cttcagccaa acatacatgc atcccatgaa gacagcggga aagccctggc tcctaagata 1560
58 tccatctctc ctgcgaacaac aaattcttcc cacttaccag atgaccctc aatccccatc 1620
59 ataagtgtg gtccaggaac cggcatagcc ccgtttattg ggttcctaca acatagagag 1680
60 aaactccaag aacaacaccc agatggaaat tttggagcaa tgtggtgtt ttttggctgc 1740

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61 aggcataagg ataggggatta tctattcaga aaagagctca gacatttcct taagcatggg 1800
62 atcttaactc atctaaagg ttccttctca agagatgctc ctgttgggga ggaggaagcc 1860
63 ccagcaaagt atgtacaaga caacatccag cttcatggcc agcaggtggc gagaatcctc 1920
64 ctccaggaga acggccatat ttatgtgtgt ggagatgcaa agaatatggc caaggatgta 1980
65 catgatgccc ttgtgcaaat aataagcaaa gaggttggag ttgaaaaact agaagcaatg 2040
66 aaaaccctgg ccactttaaa agaagaaaaa cgctaccttc aggatatttg gtcataa 2097
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69 <211> LENGTH: 698
70 <212> TYPE: PRT
71 <213> ORGANISM: Homo sapiens
73 <400> SEQUENCE: 2
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75 1 5 10 15
76 Ala Ile Ala Glu Met Cys Glu Gln Ala Val Val His Gly Phe Ser
77 20 25 30
78 Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
79 35 40 45
80 Glu Thr Ala Pro Leu Val Val Val Ser Thr Thr Gly Thr Gly Asp
81 50 55 60
82 Pro Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr
83 65 70 75 80
84 Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
85 85 90 95
86 Gly Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp
87 100 105 110
88 Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
89 115 120 125
90 Ala Asp Asp Cys Val Gly Leu Glu Leu Val Val Glu Pro Trp Ile Ala
91 130 135 140
92 Gly Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln
93 145 150 155 160
94 Glu Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Leu Arg
95 165 170 175
96 Thr Asp Leu Val Lys Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu
97 180 185 190
98 Leu Leu Arg Phe Asp Asp Ser Gly Arg Lys Asp Ser Glu Val Leu Lys
99 195 200 205
100 Gln Asn Ala Val Asn Ser Asn Gln Ser Asn Val Val Ile Glu Asp Phe
101 210 215 220
102 Glu Ser Ser Leu Thr Arg Ser Val Pro Pro Leu Ser Gln Ala Ser Leu
103 225 230 235 240
104 Asn Ile Pro Gly Leu Pro Pro Glu Tyr Leu Gln Val His Leu Gln Glu
105 245 250 255
106 Ser Leu Gly Gln Glu Glu Ser Gln Val Ser Val Thr Ser Ala Asp Pro
107 260 265 270
108 Val Phe Gln Val Pro Ile Ser Lys Ala Val Gln Leu Thr Thr Asn Asp
109 275 280 285
110 Ala Ile Lys Thr Thr Leu Leu Val Glu Leu Asp Ile Ser Asn Thr Asp
111 290 295 300

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112 Phe Ser Tyr Gln Pro Gly Asp Ala Phe Ser Val Ile Cys Pro Asn Ser
113 305 310 315 320
114 Asp Ser Glu Val Gln Ser Leu Leu Gln Arg Leu Gln Leu Glu Asp Lys
115 325 330 335
116 Arg Glu His Cys Val Leu Leu Lys Ile Lys Ala Asp Thr Lys Lys Lys
117 340 345 350
118 Gly Ala Thr Leu Pro Gln His Ile Pro Ala Gly Cys Ser Leu Gln Phe
119 355 360 365
120 Ile Phe Thr Trp Cys Leu Glu Ile Arg Ala Ile Pro Lys Lys Ala Phe
121 370 375 380
122 Leu Arg Ala Leu Val Asp Tyr Thr Ser Asp Ser Ala Glu Lys Arg Arg
123 385 390 395 400
124 Leu Gln Glu Leu Cys Ser Lys Gln Gly Ala Ala Asp Tyr Ser Arg Phe
125 405 410 415
126 Val Arg Asp Ala Cys Ala Cys Leu Leu Asp Leu Leu Leu Ala Phe Pro
127 420 425 430
128 Ser Cys Gln Pro Pro Leu Ser Leu Leu Glu His Leu Pro Lys Leu
129 435 440 445
130 Gln Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly
131 450 455 460
132 Lys Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr
133 465 470 475 480
134 Thr Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu
135 485 490 495
136 Val Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser
137 500 505 510
138 Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn
139 515 520 525
140 Ser Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly
141 530 535 540
142 Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu
143 545 550 555 560
144 Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Leu
145 565 570 575
146 Phe Phe Gly Cys Arg His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu
147 580 585 590
148 Leu Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser
149 595 600 605
150 Phe Ser Arg Asp Ala Pro Val Gly Glu Glu Glu Ala Pro Ala Lys Tyr
151 610 615 620
152 Val Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu
153 625 630 635 640
154 Leu Gln Glu Asn Gly His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met
155 645 650 655
156 Ala Lys Asp Val His Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val
157 660 665 670
158 Gly Val Glu Lys Leu Glu Ala Met Lys Thr Leu Ala Thr Leu Lys Glu
159 675 680 685
160 Glu Lys Arg Tyr Leu Gln Asp Ile Trp Ser

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163 <210> SEQ ID NO: 3
164 <211> LENGTH: 24
165 <212> TYPE: DNA
166 <213> ORGANISM: Homo sapiens
168 <400> SEQUENCE: 3
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171 <210> SEQ ID NO: 4
172 <211> LENGTH: 25
173 <212> TYPE: DNA
174 <213> ORGANISM: Homo sapiens
176 <400> SEQUENCE: 4
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180 <211> LENGTH: 23
181 <212> TYPE: DNA
182 <213> ORGANISM: Homo sapiens
184 <400> SEQUENCE: 5
185 ccctggctcc taagatatcc atc      23
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188 <211> LENGTH: 26
189 <212> TYPE: DNA
190 <213> ORGANISM: Homo sapiens
192 <400> SEQUENCE: 6
193 cgaacaacaa attctttcca cttacc      26
195 <210> SEQ ID NO: 7
196 <211> LENGTH: 23
197 <212> TYPE: DNA
198 <213> ORGANISM: Homo sapiens
200 <400> SEQUENCE: 7
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203 <210> SEQ ID NO: 8
204 <211> LENGTH: 25
205 <212> TYPE: DNA
206 <213> ORGANISM: Homo sapiens
208 <400> SEQUENCE: 8
209 atgccttgaa gtgatgagga ggttt      25
211 <210> SEQ ID NO: 9
212 <211> LENGTH: 24
213 <212> TYPE: DNA
214 <213> ORGANISM: Homo sapiens
216 <400> SEQUENCE: 9
217 ttcctacaac atagagagaa actc      24
219 <210> SEQ ID NO: 10
220 <211> LENGTH: 24
221 <212> TYPE: DNA
222 <213> ORGANISM: Homo sapiens
224 <400> SEQUENCE: 10
225 ttgcacaagg gcatcatgta catc      24

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Input Set : A:\seqlist.txt
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227 <210> SEQ ID NO: 11
228 <211> LENGTH: 25
229 <212> TYPE: DNA
230 <213> ORGANISM: Homo sapiens
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235 <210> SEQ ID NO: 12
236 <211> LENGTH: 23
237 <212> TYPE: DNA
238 <213> ORGANISM: Homo sapiens
240 <400> SEQUENCE: 12
241 cttgcacacg aatatggtct ggg          23
243 <210> SEQ ID NO: 13
244 <211> LENGTH: 23
245 <212> TYPE: DNA
246 <213> ORGANISM: Homo sapiens
248 <400> SEQUENCE: 13
249 tggcatcacc tgcacacctg agg          23
251 <210> SEQ ID NO: 14
252 <211> LENGTH: 25
253 <212> TYPE: DNA
254 <213> ORGANISM: Homo sapiens
256 <400> SEQUENCE: 14
257 gatgtacctg taaatattct ggggg          25
259 <210> SEQ ID NO: 15
260 <211> LENGTH: 24
261 <212> TYPE: DNA
262 <213> ORGANISM: Homo sapiens
264 <400> SEQUENCE: 15
265 aatccacggc tcaaccacaa gtgc          24
267 <210> SEQ ID NO: 16
268 <211> LENGTH: 25
269 <212> TYPE: DNA
270 <213> ORGANISM: Homo sapiens
272 <400> SEQUENCE: 16
273 ctcgaaatta accctcacta aaggg          25
275 <210> SEQ ID NO: 17
276 <211> LENGTH: 23
277 <212> TYPE: DNA
278 <213> ORGANISM: Homo sapiens
280 <400> SEQUENCE: 17
281 aaccataacc gcaggtgagc aaa          23
283 <210> SEQ ID NO: 18
284 <211> LENGTH: 29
285 <212> TYPE: DNA
286 <213> ORGANISM: Homo sapiens
288 <400> SEQUENCE: 18
289 tttagtactt tcagtcaaaa aagcttaat          29
291 <210> SEQ ID NO: 19

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VERIFICATION SUMMARY DATE: 05/05/2000
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